

AMENDMENTS TO THE SPECIFICATION

Please amend the specification at line 17, page 10 in the paragraph which begins at line 26 on page 9, as follows:

“According to the present invention, the term “functional variant” is understood as meaning a nucleic acid which is related functionally to the *Tetrahymena* delta-6-desaturase. Examples of related nucleic acids are, for example, nucleic acids from other ciliate cells, or allelic or degenerate variants. The invention likewise encompasses functional variants of the nucleic acids according to the invention which, because of the unusual codon usage (see: Wuitschick JD, Karrer KM (1999) Analysis of genomic G + C content, codon usage, initiator codon context and translation termination sites in *Tetrahymena thermophila*. J. Eukaryot. Microbiol. 1999 46(3):239-47), require an adaptation of the nucleic acids according to the invention in selected expression systems. On the one hand, this relates to the replacement of the codons TAA and TAG, which encode glutamine in ciliates and which are stop codons in most other expression systems, with CAA and CAG. In addition to this, the skilled person is familiar with optimally adapting the nucleic acids according to the invention to the given particular codon preference (what is termed codon usage) of different expression systems. The nucleic acids can be modified in a known manner by specifically substituting bases or else the nucleic acid which is required is obtained from artificially prepared oligonucleotides. The adaptation of the sequence can be carried out, for example, on the basis of the known codon usage tables (e.g. on the Internet: Codon usage tabulated from Genbank) [~~http://www.dna.affrc.go.jp/~nakamura/CUTG.html~~] for the preferred expression systems. The present invention also encompasses variants of nucleic acids which only contain parts of the nucleic acid.”

Please amend the specification at lines 24-25 on page 24 in the paragraph which begins at line 18 on page 24, as follows:

“SEQ ID NO:2: The protein sequence of the *Tetrahymena* delta-6-desaturase which is deduced from SEQ ID No.: 1 taking into consideration the special ciliate codon usage (Wuitschick JD, Karrer KM (1999) or CUTG (codon usage tabulated from Genbank) [~~http://www.dna.affrc.go.jp/~nakamura/CUTG.html~~]).”

Please amend the specification at line 11 on page 27 in the paragraph which begins at line 35 on page 26, as follows:

“By comparing sequences of known desaturases, it was possible to identify conserved regions. While taking into consideration the special ciliate codon usage and/or *Tetrahymena* codon usage, it was possible to design PCR primers for the particularly strongly conserved amino acid regions WWKWNHNAHH (SEQ ID No.: 4) and GGLQFQIEHHLFP (SEQ ID No.: 5) (Wuitschick JD, Karrer KM (1999) Analysis of genomic G + C content, codon usage, initiator codon context and translation termination sites in *Tetrahymena thermophila*. J. Eukaryot. Microbiol. 46(3):239-47; Martindale (1989) J. Protozool. 36, 1:29-34, CUTG, (Codon Usage Tabulated from Genbank) [~~http://www.dna.affrc.go.jp/~nakamura/CUTG.html~~]).”

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